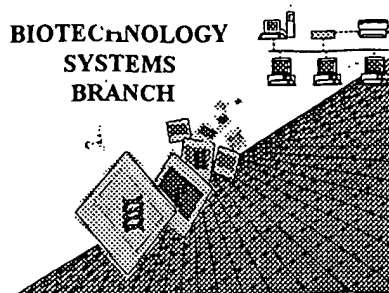# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/900, 038_

Source: _OIPE_

Date Processed by STIC: _7/24/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,038

DATE: 07/24/2001
TIME: 11:10:29

pp 1-3

*Does Not Comply
Corrected Diskette Needed*

Input Set : A:\766.53 CRF.txt
Output Set: N:\CRF3\07242001\I900038.raw

```
 3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
 5 <120> TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
 7 <130> FILE REFERENCE: 11328
 9 <140> CURRENT APPLICATION NUMBER: US/09/900,038
 9 <141> CURRENT FILING DATE: 2001-07-09
 9 <150> PRIOR APPLICATION NUMBER: JP 2001-392
10 <151> PRIOR FILING DATE: (2001-1-5)  2001-01-05 ← use this date format
12 <160> NUMBER OF SEQ ID NOS: 8
14 <170> SOFTWARE: PatentIn Ver. 2.0
```

W--> (annotation on line 10)

ERRORED SEQUENCES

```
16 <210> SEQ ID NO: 1      ← mandatory response needed - 3/3 shown (p2)
17 <211> LENGTH:
18 <212> TYPE: PRT
19 <213> ORGANISM: Streptococcus agalactiae Type Ib
20 <400> SEQUENCE: 1
21  Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
22   1               5                  10                  15
24  Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
25               20                  25                  30
27  Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
28           35                  40                  45
30  Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu
31       50                  55                  60
33  Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
34   65                  70                  75                  80
36  Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
37               85                  90                  95
39  Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
40               100                 105                 110
42  Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
43           115                 120                 125
45  Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
46       130                 135                 140
48  Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
49   145                 150                 155                 160
51  Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
52               165                 170                 175
54  Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp
55               180                 185                 190
57  Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
58           195                 200                 205
60  Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
61       210                 215                 220
63  Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr
```

```
  64    225                    230                   235                    240
  66    Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr
  67                       245                   250                    255
  69    Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile
  70                       260                   265                    270
  72    Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro
  73               275                   280                   285
  75    Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys
  76           290                   295                   300
  78    Leu Phe Gly Gly Glu Lys Gln Ser Asp
E--> 79    305                   310       313
  81    <210> SEQ ID NO: 2
  82    <211> LENGTH: 939 shown (p.3)
  83    <212> TYPE: DNA
  84    <213> ORGANISM: Streptococcus agalactiae Type Ib
  85    <400> SEQUENCE: 2
  86    atg aat tat agt atc att atg tcg gta tat aat gag cct tta aat tat    48
  87    Met Asn Tyr Ser Ile Ile Met Ser Val Tyr Asn Glu Pro Leu Asn Tyr
  88     1               5                   10                  15
  90    gtg aga gat tca gta gaa tct ata tta aat caa acg ctt act gat ttt    96
  91    Val Arg Asp Ser Val Glu Ser Ile Leu Asn Gln Thr Leu Thr Asp Phe
  92                   20                  25                  30
  94    gag ttc ata att gtc att gat aat cca agt aga ggt gat tta aag caa   144
  95    Glu Phe Ile Ile Val Ile Asp Asn Pro Ser Arg Gly Asp Leu Lys Gln
  96               35                  40                  45
  98    ttc tta aca gaa tat tca gtt gta gat aat aga ata aaa atc ttg ctt   192
  99    Phe Leu Thr Glu Tyr Ser Val Val Asp Asn Arg Ile Lys Ile Leu Leu
 100           50                  55                  60
 102    aat gaa gaa aat att ggt tta gca tca agt ttg aac aaa gcg gtg aaa   240
 103    Asn Glu Glu Asn Ile Gly Leu Ala Ser Ser Leu Asn Lys Ala Val Lys
 104        65                  70                  75                  80
 106    att tct aag gga gaa tat att ttt aga atg gat gct gat gat att tca   288
 107    Ile Ser Lys Gly Glu Tyr Ile Phe Arg Met Asp Ala Asp Asp Ile Ser
 108                       85                  90                  95
 110    tat cca agt aga ttt gat aag caa att cgt ttt atg gag gaa aat tca   336
 111    Tyr Pro Ser Arg Phe Asp Lys Gln Ile Arg Phe Met Glu Glu Asn Ser
 112               100                 105                 110
 114    ttg gat ttc tca gca act cta ata gaa ttg ata gac caa aaa gga aat   384
 115    Leu Asp Phe Ser Ala Thr Leu Ile Glu Leu Ile Asp Gln Lys Gly Asn
 116           115                 120                 125
 118    tta gta tat aaa caa cga gaa agt aat aaa ata tac tta act aat gat   432
 119    Leu Val Tyr Lys Gln Arg Glu Ser Asn Lys Ile Tyr Leu Thr Asn Asp
 120        130                 135                 140
 122    ata cgg aag atg tta ttg aat aga tct ata ctt gcc cac cca acg tgg   480
 123    Ile Arg Lys Met Leu Leu Asn Arg Ser Ile Leu Ala His Pro Thr Trp
 124    145                 150                 155                 160
 126    tgc gta aaa aag aaa gtt ttc gat aag tta atg gga tat aga gat tta   528
 127    Cys Val Lys Lys Lys Val Phe Asp Lys Leu Met Gly Tyr Arg Asp Leu
 128               165                 170                 175
```

```
130    gta cct gtt gaa gat tat gat ttt gca ata aga gga gct ctg gct gat    576
131    Val Pro Val Glu Asp Tyr Asp Phe Ala Ile Arg Gly Ala Leu Ala Asp
132            180                 185                 190
134    ttc aaa atc ggc tta ctc aat aaa gta ctt tta cag tat aga tta aac    624
135    Phe Lys Ile Gly Leu Leu Asn Lys Val Leu Leu Gln Tyr Arg Leu Asn
136            195                 200                 205
138    gag aat gga ata tca caa acc aat aag ttt aag caa tat att tac tca    672
139    Glu Asn Gly Ile Ser Gln Thr Asn Lys Phe Lys Gln Tyr Ile Tyr Ser
140            210                 215                 220
142    gct att tta caa gat ttt tat aaa gaa aaa tct tat att gat atc aca    720
143    Ala Ile Leu Gln Asp Phe Tyr Lys Glu Lys Ser Tyr Ile Asp Ile Thr
144    225                 230                 235                 240
146    aaa att act aat tac ttt caa gag tat gtg ata aag aaa cgc tat act    768
147    Lys Ile Thr Asn Tyr Phe Gln Glu Tyr Val Ile Lys Lys Arg Tyr Thr
148                245                 250                 255
150    cag caa gag ctc tct aaa tat ttt gag cta aaa tct acc cct agt att    816
151    Gln Gln Glu Leu Ser Lys Tyr Phe Glu Leu Lys Ser Thr Pro Ser Ile
152            260                 265                 270
154    act att aga aaa cta tat att tgt tta tat tta tac ttt aag tct ccc    864
155    Thr Ile Arg Lys Leu Tyr Ile Cys Leu Tyr Leu Tyr Phe Lys Ser Pro
156            275                 280                 285
158    ttg gtt agg agg tta tta ata aat gat att aat att tta gta ctg aaa    912
159    Leu Val Arg Arg Leu Leu Ile Asn Asp Ile Asn Ile Leu Val Leu Lys
160            290                 295                 300
162    ttg ttt gga gga gag aaa caa agt gac                                 939
163    Leu Phe Gly Gly Glu Lys Gln Ser Asp
164    305                 310
```

730 <210> SEQ ID NO: 8
731 <211> LENGTH: 32
732 <212> TYPE: DNA
733 <213> ORGANISM: Artificial Sequence
734 <220> FEATURE:
735 <223> OTHER INFORMATION: Synthetic DNA
736 <400> SEQUENCE: ← 8 (insert)
737   ccggaattcg aaaaggtaaa gtgtctccga aa   32

VERIFICATION SUMMARY   DATE: 07/24/2001
PATENT APPLICATION: **US/09/900,038**   TIME: 11:10:30

Input Set : **A:\766.53 CRF.txt**
Output Set: **N:\CRF3\07242001\I900038.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:20 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:313 SEQ:1
L:85 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:939 SEQ:2
L:693 M:283 W: Missing Blank Line separator, <220> field identifier
L:695 M:283 W: Missing Blank Line separator, <400> field identifier
L:704 M:283 W: Missing Blank Line separator, <220> field identifier
L:706 M:283 W: Missing Blank Line separator, <400> field identifier
L:714 M:283 W: Missing Blank Line separator, <220> field identifier
L:716 M:283 W: Missing Blank Line separator, <400> field identifier
L:724 M:283 W: Missing Blank Line separator, <220> field identifier
L:726 M:283 W: Missing Blank Line separator, <400> field identifier
L:734 M:283 W: Missing Blank Line separator, <220> field identifier
L:736 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:7
L:736 M:283 W: Missing Blank Line separator, <400> field identifier
```